

## SEQUENCE LISTING

&lt;110&gt; Folks, Thomas M.

&lt;120&gt; LIVE REPLICATING SPUMAVIRUS VECTOR

&lt;130&gt; 14114.0373U2

&lt;140&gt; Unassigned

&lt;141&gt; 2004-12-27

&lt;150&gt; PCT/US03/20325

&lt;151&gt; 2003-06-27

&lt;150&gt; 60/392,630

&lt;151&gt; 2002-06-27

&lt;160&gt; 8

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 16360

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 1

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acaatagcag	tctctatttg	tgtgcatcaa	aggatagatg	taaaagacac	caaggaagcc	14220
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tactttatta	agtaaaagga	tttgtatatt	agccttgcta	agggagacat	ctagtatat	16140
aagtgtgaac	tacacttatc	ttaaatgatg	ttaactcctta	ggataatcaa	tatacaaaat	16200
tccatgacaa	gatccacagg	acgggtgtgg	tcgccatgat	cgcgtagtcg	atagtggctc	16260
caagtagcga	agcgagcagg	actgggaggc	ggccaaagcg	gtcggacagt	gctccgagaa	16320

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16360

<210> 2  
<211> 1503  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 2  
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ttaaggccag ggggaaagaa acaatataaa ctaaaacata tagtatgggc aagcagggag 120  
ctagaacgat tcgcagttaa tcctggcctt ttagagacat cagaaggctg tagacaaata 180  
ctgggacagc tacaaccatc ccttcagaca ggatcagaag aacttagatc attatataat 240  
acaatagcag tcctctattg tgtgcatcaa aggatagatg taaaagacac caaggaagcc 300  
ttagataaga tagaggaaga gcaaaacaaa agtaagaaaa aggcacagca agcagcagct 360  
gacacaggaa acaacagcca ggtcagccaa aattacccta tagtgcagaa cctccagggg 420  
caaattggtac atcaggccat atcacctaga acttttaaat catgggtaaa agtagtagaa 480  
gagaaggctt tcagcccaga agtaataccc atgttttcag cattatcaga aggagccacc 540  
ccacaagatt taaataccat gctaaacaca gtggggggac atcaagcagc catgcaaattg 600  
ttaaagagaa ccatcaatga ggaagctgca gaatgggata gattgcattcc agtgcattgca 660  
gggcctattg caccaggcca gatgagagaa ccaaggggaa gtgacatagc aggaactact 720  
agtacccttc aggaacaaat aggatggatg acacataatc cacctatccc agtaggagaa 780  
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agcattcttg acataagaca aggaccaaag gaacccttta gagactatgt agaccgattc 900  
tataaaactc taagagccga gcaagcttca caagaggtaa aaaattggat gacagaaacc 960  
ttgttggtcc aaaatgcgaa ccagattgt aagactattt taaaagcatt gggaccagga 1020  
gcgacactag aagaaatgat gacagcatgt cagggagtgg ggggacccgg ccataaagca 1080  
agagtgttgg ctgaagcaat gagccaagta acaaatccag ctaccataat gatacagaaa 1140  
ggcaatttta ggaaccaaag aaagactgtt aagtgtttca attgtggcaa agaagggcac 1200  
atagccaaaa attgcagggc ccctaggaaa aagggtgtt ggaaatgtgg aaaggaagga 1260  
caccaaatga aagattgtac tgagagacag gctaattttt tagggaagat ctggccttcc 1320  
cacaaggga ggccaggga ttttcttcag agcagaccag agccaacagc cccaccagaa 1380  
gagagcttca gggttgggga agagacaaca actccctctc agaagcagga gccgatagac 1440  
aaggaactgt atccttttagc ttccctcaga tcactctttg gcagcgaccc ctcgtcacia 1500  
taa 1503

<210> 3  
<211> 500  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 3  
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1 5 10 15  
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Gln Tyr Lys Leu Lys  
20 25 30  
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro  
35 40 45  
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu  
50 55 60  
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn  
65 70 75 80

Thr	Ile	Ala	Val	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Asp	Val	Lys	Asp	85	90	95
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Gln	Asn	Lys	Ser	Lys	100	105	110	
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	Asn	Asn	Ser	Gln	Val	115	120	125
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Leu	Gln	Gly	Gln	Met	Val	His	130	135	140
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	145	150	155
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	165	170	175
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	180	185	190
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	195	200	205
Ala	Ala	Glu	Trp	Asp	Arg	Leu	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	210	215	220
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	225	230	235
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	His	Asn	Pro	Pro	Ile	245	250	255
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	260	265	270
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	275	280	285
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	290	295	300
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	305	310	315
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	325	330	335
Leu	Gly	Pro	Gly	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	340	345	350
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	355	360	365
Gln	Val	Thr	Asn	Pro	Ala	Thr	Ile	Met	Ile	Gln	Lys	Gly	Asn	Phe	Arg	370	375	380
Asn	Gln	Arg	Lys	Thr	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly	His	385	390	395
Ile	Ala	Lys	Asn	Cys	Arg	Ala	Pro	Arg	Lys	Lys	Gly	Cys	Trp	Lys	Cys	405	410	415
Gly	Lys	Glu	Gly	His	Gln	Met	Lys	Asp	Cys	Thr	Glu	Arg	Gln	Ala	Asn	420	425	430
Phe	Leu	Gly	Lys	Ile	Trp	Pro	Ser	His	Lys	Gly	Arg	Pro	Gly	Asn	Phe	435	440	445
Leu	Gln	Ser	Arg	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Glu	Glu	Ser	Phe	Arg	450	455	460
Phe	Gly	Glu	Glu	Thr	Thr	Pro	Ser	Gln	Lys	Gln	Glu	Pro	Ile	Asp	465	470	475	
Lys	Glu	Leu	Tyr	Pro	Leu	Ala	Ser	Leu	Arg	Ser	Leu	Phe	Gly	Ser	Asp	485	490	495
Pro	Ser	Ser	Gln	500														

<210> 4

<211> 512

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 4

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Glu	Lys	Ile	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Leu	Lys	20	25	30	
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro	35	40	45	
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu	50	55	60	
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn	65	70	75	80
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp	85	90	95	
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Ser	Lys	100	105	110	
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Ser	Gln	Val	115	120	125	
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His	130	135	140	
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu	145	150	155	160
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser	165	170	175	
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly	180	185	190	
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu	195	200	205	
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala	210	215	220	
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr	225	230	235	240
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile	245	250	255	
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys	260	265	270	
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly	275	280	285	
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu	290	295	300	
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr	305	310	315	320
Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala	325	330	335	
Leu	Gly	Pro	Ala	Ala	Thr	Leu	Glu	Glu	Met	Met	Thr	Ala	Cys	Gln	Gly	340	345	350	
Val	Gly	Gly	Pro	Gly	His	Lys	Ala	Arg	Val	Leu	Ala	Glu	Ala	Met	Ser	355	360	365	
Gln	Val	Thr	Asn	Ser	Ala	Thr	Ile	Met	Met	Gln	Arg	Gly	Asn	Phe	Arg	370	375	380	
Asn	Gln	Arg	Lys	Ile	Val	Lys	Cys	Phe	Asn	Cys	Gly	Lys	Glu	Gly	His	385	390	395	400
Ile	Ala	Arg	Asn	Cys	Arg	Ala	Pro	Arg	Lys	Lys	Gly	Cys	Trp	Lys	Cys	405	410	415	
Gly	Lys	Glu	Gly	His	Gln	Met	Lys	Asp	Cys	Thr	Glu	Arg	Gln	Ala	Asn	420	425	430	
Phe	Leu	Gly	Lys	Ile	Trp	Pro	Ser	Tyr	Lys	Gly	Arg	Pro	Gly	Asn	Phe	435	440	445	



Leu	Gln	Ser	Arg	Pro	Glu	Pro	Thr	Ala	Pro	Pro	Phe	Leu	Gln	Ser	Arg
450						455					460				
Pro	Glu	Pro	Thr	Ala	Pro	Pro	Glu	Glu	Ser	Phe	Arg	Ser	Gly	Val	Glu
465					470					475					480
Thr	Thr	Thr	Pro	Ser	Gln	Lys	Gln	Glu	Pro	Ile	Asp	Lys	Glu	Leu	Tyr
				485					490					495	
Pro	Leu	Thr	Ser	Leu	Arg	Ser	Leu	Phe	Gly	Asn	Asp	Pro	Ser	Ser	Gln
			500					505					510		

<210> 5

<211> 512

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 5

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Glu	Lys	Val	Arg	Leu	Arg	Pro	Gly	Gly	Lys	Lys	Lys	Tyr	Lys	Leu	Lys
			20					25					30		
His	Ile	Val	Trp	Ala	Ser	Arg	Glu	Leu	Glu	Arg	Phe	Ala	Val	Asn	Pro
		35					40					45			
Gly	Leu	Leu	Glu	Thr	Ser	Glu	Gly	Cys	Arg	Gln	Ile	Leu	Gly	Gln	Leu
		50				55					60				
Gln	Pro	Ser	Leu	Gln	Thr	Gly	Ser	Glu	Glu	Leu	Arg	Ser	Leu	Tyr	Asn
65					70					75					80
Thr	Val	Ala	Thr	Leu	Tyr	Cys	Val	His	Gln	Arg	Ile	Glu	Ile	Lys	Asp
				85					90					95	
Thr	Lys	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Glu	Glu	Gln	Asn	Lys	Ser	Lys
			100					105					110		
Lys	Lys	Ala	Gln	Gln	Ala	Ala	Ala	Asp	Thr	Gly	His	Ser	Ser	Gln	Val
		115					120					125			
Ser	Gln	Asn	Tyr	Pro	Ile	Val	Gln	Asn	Ile	Gln	Gly	Gln	Met	Val	His
		130				135					140				
Gln	Ala	Ile	Ser	Pro	Arg	Thr	Leu	Asn	Ala	Trp	Val	Lys	Val	Val	Glu
145					150					155					160
Glu	Lys	Ala	Phe	Ser	Pro	Glu	Val	Ile	Pro	Met	Phe	Ser	Ala	Leu	Ser
				165					170					175	
Glu	Gly	Ala	Thr	Pro	Gln	Asp	Leu	Asn	Thr	Met	Leu	Asn	Thr	Val	Gly
		180						185					190		
Gly	His	Gln	Ala	Ala	Met	Gln	Met	Leu	Lys	Glu	Thr	Ile	Asn	Glu	Glu
		195					200						205		
Ala	Ala	Glu	Trp	Asp	Arg	Val	His	Pro	Val	His	Ala	Gly	Pro	Ile	Ala
		210				215					220				
Pro	Gly	Gln	Met	Arg	Glu	Pro	Arg	Gly	Ser	Asp	Ile	Ala	Gly	Thr	Thr
225					230					235					240
Ser	Thr	Leu	Gln	Glu	Gln	Ile	Gly	Trp	Met	Thr	Asn	Asn	Pro	Pro	Ile
				245					250					255	
Pro	Val	Gly	Glu	Ile	Tyr	Lys	Arg	Trp	Ile	Ile	Leu	Gly	Leu	Asn	Lys
		260						265					270		
Ile	Val	Arg	Met	Tyr	Ser	Pro	Thr	Ser	Ile	Leu	Asp	Ile	Arg	Gln	Gly
		275					280					285			
Pro	Lys	Glu	Pro	Phe	Arg	Asp	Tyr	Val	Asp	Arg	Phe	Tyr	Lys	Thr	Leu
	290					295					300				
Arg	Ala	Glu	Gln	Ala	Ser	Gln	Glu	Val	Lys	Asn	Trp	Met	Thr	Glu	Thr
305					310					315					320

Leu	Leu	Val	Gln	Asn	Ala	Asn	Pro	Asp	Cys	Lys	Thr	Ile	Leu	Lys	Ala		
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